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OM protein - protein search, using sw model
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Perfect score:
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Listing first 45 summaries
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     SPTREMBL_15:*

1: sp_acchea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_fodent:*
12: sp_vertebrate
13: sp_vertebrate
14: sp_unclassifi
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Gapop 10.0 , Gapext 0.5
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53
1 CXXXCXXXXXXXXXXXXXXXXX 21
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sp_organelle:*
sp_phage:*
sp_plant:*
sp_fodent:*
sp_virus:*
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                                                                                                                       sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PRT; 32 AA. 8, Created) 8, Last sequence up 8, Last annotation R) (FRAGMENT).		21 30 ·	; Score 53; DB Pred. No. 61; 17; Mismatches	 F492F6F29C2C5CE	O., Murayama Y.; andem repeats of	Created) Last sequence u Last annotation (FRAGMENT). (Crailed galago) (Craniata; Ver (Strepsirhini;	PRT; 32 AA.	ALIGNMENTS	Q9TUH0 Q9TUG9 Q28834 Q84631	Q9XVX3 Q9TUH2 Q9TUH1	077494 028576	Q9TUG7 Q9TUG6 Q9U1U5	Q18157 Q18157 Q9TUG8	Q9N3Z7 Q9W3A7	Q02393 Q9TUG5	014633 046202 095176	Q9VUV1	Q9NLE3
AA. update) on update)			6; Length 32; 0; Indels 0; Gaps 0;	EC CRC64;	primate D4 dopamine	pdate) update) (Otolemur crassicaudatus). tebrata; Euteleostomi; Galagonidae; Otolemur.			lobate lobate yctola aramec	hylobates hylobates	tarsius ba		200	caenorhabd drosophila	hylobates	homo sapi drosophil homo sapi	. e #	leishmani

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Q16861;
01-NOV-1996 (TrEMBLrel 01, Created
01-NOV-1996 (TrEMBLrel 07, Last se
01-AUG-1998 (TREMBLEL 07, Last an
CYSTELUE-RICH PROTEIN (FRAGMENT).
Homo sapiens (Human)
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Q9U623;
Q1-MAY-2000
SEQUENCE FROM N.A.
TISSUE-THORACIC GANGLIA;
SKORUPSKI P., Dawbarn D.;
Submitted (OCT-1999) to the
EMBL; AF199482; AAF07215.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
Astacoidea; Astacidae; Pacifastacus.
                                                                                                                                                                                                           METALLOTHIONEIN.
Pacifastacus leniusculus (Signal crayfish).
                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2000 (TrEMBLrel. 15,
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                                                                                                                            NCBI_TaxID=6720;
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
EMBL; U63332; AAB05810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Primates 39:217-224(1998).
EMBL; AB016202; BAA32040.1;
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Mammalia; Eutheria;
NCBI_TaxID=9447;
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01-JAN-1998 (TREMBLRE1. C
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INTERPRO; IPR002045; -.
INTERPRO; IPR003019; -.
IPRAM; PF00131; metalthio; 1.
PRINTS; PR00858; MTCRUSTACEAN.
SEQUENCE 58 AA; 6008 MW; 57
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Q9M402;
01-OCT-2000
01-OCT-2000
01-OCT-2000
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EMBL; AJ276118; CABB3040.1; -.
NON_TER 62 62
SEQUENCE 62 AA; 7158 MW; 10690D53F7700
Li Y., Lu Z., Sun L., Ropp S., Kutish "Analysis of 74 kb of DNA located at t chlorella virus PBCV-1 genome.";
                                                                                                                 viruses; dsDNA vi
NCBI_TaxID=10506;
                                                              SEQUENCE FROM N.A. MEDLINE=98022962;
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Magnoliophyta; eudicotyledons; core eudicot
Fabales; Fabaceae; Papilionoldeae; Glycine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morassutti C., Marchetti S., De Amicis F., Zaina G., Zanet Morassutti C., Marchetti S., De Amicis F., Zaina G., Zanet "Expression and purification of the antimicrobial peptide tobacco transgenic plants by SceVMA-intein system."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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ses, no RNA stage;
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dons; core eudicots; Rosidae;
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Pred. N
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10690D53F7700443 CRC64;
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                        h G.F., Rock D.L.,
the right end of
                                                                                                                                                  (PBCV-1).
Phycodnaviridae;
                                                                                                                                                                                                                                                                                                                                 66
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e; eurosids I;
                        , Van Etten J.L.;
the 330-kb
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                       RA Abrill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Botchan M.R., Bouck J., Brokstein P., Brottler P., Rottler P., Shotchan M.R., Bouck J., Brokstein P., Brottler R., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M., Burtis K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W., RA, Bodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Dunkov B.C., Dunn P., RA Dodson K.J., Babrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA, Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA, Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA, Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA, Liu X., Mattei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA, Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA, Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA, Merxulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA, Aultsin D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA, Mentert K., Remington K.S., Janders R.D.C., Scheeler F., Shen H., RA, Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T., RA, Palazzolo M., Pittman G.S., Stapleton M., Strong R., Sun E., Shen H., Barn R., Sunders R.D.C., Scheeler F., Shen H., RA, Shue B.C., Yen R., Ferran D.A., Weinstock G.M., Weissenbach J., RA, Warss S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA, Liu X., Yang S., Yao Q.A., Yang
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01-MAY-2000
01-JUN-2000
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EMBL; U42580; AAC97026.1; -.
SEQUENCE 66 AA; 7112 MW;
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               FBgn0004175; Mst84Dd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              melanogaster (Fruit fly)
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01-AUG-1998
01-AUG-1998
01-OCT-2000
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062554;
                                                           Barsyte D., White K.N., Low Submitted (APR-1998) to the EMBL; AJ005453; CAA06550.1;
                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0875; MTMOLLUSC.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
SEQUENCE 73 AA; 7220 MW; 76797FB0FCD7B3B2 CRC64;
                                                                                                                                              Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barsyte D., White K.N., Lovejoy D.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=DIGESTIVE GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mytiloidea; Mytilidae;
NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_2
SEQUENCE 72 AA; 6840 MW; 8CE37449E5F88ABA
         PRINTS; PR00875; MTMOLLUSC.
                     PFAM; PF00131; metalthio;
                                                                                             TISSUE=DIGESTIVE GLAND;
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=6550;
                                                                                                                                      Mytiloidea; Mytilidae;
                                                                                                                                                                    METALLOTHIONEIN 10 II.
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4; Conservative
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 PS00022;
                              IPR003019; -
                                                   IPR000561;
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                                         IPR001008; -
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                                                                                                                                                                                                                                                                                                                    Conservative
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EGF_1; UNKNOWN_1.
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                                                                                                                                      Mytilus
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                                                                                  Lovejoy D.A.;
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Pred. No.
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                                                                                                                                                Bivalvia;
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                                                                                                                                              Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                       AΑ
                                                                                                                                                                                                                                                                                                                                       DB 5; Length 73;
                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 72;
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                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                  0;
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SO

SEQUENCE

73

AA;

7153 MW;

20CFA4CB3A0CDE19 CRC64;

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RESULT
Q9VIA1
                                                                            RA Ballew R.M., Basua A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., J., Evangelista C.C., Ferriaz C., Ferriar S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Horstin D., Houston K.A., Howland T.J., Wei M.-H., Lbegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Lbegwam C.,
RA Kinmel B.E., Kodlra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentariolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Ra Mang Z.-Y., Wassarman D.A., Weinstock G.M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong W., Zhou X., Smith H.O.,
RA Zheng X., Saperi J.S., Zha M., Zhang G., Zhao Q., Zheng L.,
Ra Ciphia R., Sha Mershoh
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Diracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muso-
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MST84DB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000
01-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                              INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 CGDACKCSGADCKCSGCKVVC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
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4; Conser
PS00198;
                                                              FBgn0004173; Mst84Db
                                              IPR001450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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  4FE4S_FERREDOXIN; UNKNOWN_4.
6725 MW; CC64F0F7A7E7CABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
19.0%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 53; D
Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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RESULT
Q16274
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Q9N0X1
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Best Local
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Best Local Similarity
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                                                                                                                                                                     Q16274
Q16274;
Q1-00V-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                        NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9NOX1 PRELIMINARY;
Q9NOX1;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                              Bowden P.E.,
J. Dermatol.
                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                             TYPE II HAIR KERATIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUTATIVE EPIDERMAL GROWTH FACTOR RECEPTOR (FRÂGMENT).
OryCtolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
SEQUENCE
          NON_TER
                             PROSITE;
                                      PFAM; PF00038; filament; 1.
                                                                                        Bowden P.
                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Submatted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF243516; AAF65771.1; -
                                                        -!- SIMILARITY: TO ALL OTHER INTERMEDIATE FILAMENT PROTEINS EMBL; S75796; AAB32813.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=SCLERA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9986;
                   [ntermediate
                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                 Thu M.K., Beuerman R. "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                 NTERPRO;
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                                                                                                  FROM N.A.
                              PS00226;
                                                 IPR001664; -
81
                                                                                                                                                                                                                                                                                                                                                         74
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74
1 AA;
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                                                                              Sci.
                  filament;
                                                                              Hainey S., Parker G., Sci. 0:0-0(1994).
AA;
          ; IF; 1.
8244 MW;
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8155
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19.0%;
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Last
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Last annotation update)
                                                                                                                                                                                          Created)
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5F0A3D7735A5B03C CRC64;
                                                                                                                                                                                                                                                                                                                   Pred.
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                  coil; Heptad
                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                        Score
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                                                                                                                                                                                                                                                                                                                   NO.
                                                                                       Hodgins M.B.;
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                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                      0
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Query Match Best Local Similarity

100.0%; 19.0%;

Score 53; DB 4 Pred. No. 1e+02;

Length 81;

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RESULT
072913
ID
072913
ID
07
DT
07

    RESULT
Q67593
ID Q67
AC Q67
DT Q1
DT Q1
DT Q1
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Q9JM45
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Matches 4
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Best Local Similarity
Matches 4; Conserv
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  Q67593;
Q67593;
Q1-NOV-1996
Q1-NOV-1998
Q1-NOV-1998
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072913;
01-AUG-1998
01-AUG-1998
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                Sugimoto K., Hirochika H., Minobe Y., Kawamata H., Hibi Yamashita S., Tsuchizaki T.; Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases. EMBL; D00800; BAA25577.1; -. SEQUENCE 84 AA; 8721 MW; B57A04C249776B1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Jin C., Lau A.F.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF038507; AAF28736.1; -.
SEQUENCE 83 AA; 8909 MW; 275B78E46428A3DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09JM45;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miscanthus streak virus.
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORF V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9JM45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10825;
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pes 4; Conservative
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Search completed:
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Matches 4; Conserv
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Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; D01030; BAA00837.1; -.
SEQUENCE 84 AA; 8751 MW; A8CCDFB249776B1C CRC64;
                                                                                                                                                                                                                                                        Viruses; ssDNA viruses; NCBI_TaxID=10825;
                                                                                                                                                                                                              Davies J.W.;
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Miscanthus streak virus
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